

## SEQUENCE LISTING

&lt;110&gt; KAO CORPORATION

&lt;120&gt; Mutant alkali cellulase

&lt;130&gt; P

&lt;150&gt; JP P2002-124474

&lt;151&gt; 2002-04-25

&lt;160&gt; 6

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 824

&lt;212&gt; PRT

&lt;213&gt; Bacillus sp.KSM-S237

&lt;400&gt; 1

Met Met Leu Arg Lys Lys Thr Lys Gln Leu Ile Ser Ser Ile Leu Ile

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10

15

Leu Val Leu Leu Leu Ser Leu Phe Pro Ala Ala Leu Ala Ala Glu Gly

20

25

30

Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp Asn Val

35

40

45

Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val Asp Gly

50	55	60	
Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu Arg Gly			
65	70	75	80
Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn Asp Asn			
85	90	95	
Ala Tyr Lys Ala Leu Ser Asn Asp Trp Asp Ser Asn Met Ile Arg Leu			
100	105	110	
Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Thr Asn Pro Glu Leu Ile			
115	120	125	
Lys Gln Arg Val Ile Asp Gly Ile Glu Leu Ala Ile Glu Asn Asp Met			
130	135	140	
Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro Arg Asp			
145	150	155	160
Pro Val Tyr Ala Gly Ala Lys Asp Phe Phe Arg Glu Ile Ala Ala Leu			
165	170	175	
Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu Pro Ser			
180	185	190	
Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu Gly Trp			
195	200	205	
Lys Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu Arg Lys			
210	215	220	
Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp			
225	230	235	240
Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His			
245	250	255	
Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala Ser Thr			
260	265	270	

Glu Ser Tyr Pro Ser Glu Thr Pro Asn Ser Glu Arg Gly Asn Val Met			
275	280	285	
Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe Ala Thr			
290	295	300	
Glu Trp Gly Thr Ser Gln Ala Ser Gly Asp Gly Gly Pro Tyr Phe Asp			
305	310	315	320
Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile Ser Trp			
325	330	335	
Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly Ala Phe Thr			
340	345	350	
Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp Pro Gly Pro			
355	360	365	
Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly Glu Tyr Val			
370	375	380	
Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp Arg Thr Lys			
385	390	395	400
Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys Gln Gly Phe			
405	410	415	
Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala Val Asp Asn			
420	425	430	
Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser Asn Asp Val			
435	440	445	
Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala Asn Gly Trp			
450	455	460	
Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met Asp Val			
465	470	475	480
Ile Val Asp Glu Pro Thr Thr Val Ala Ile Ala Ala Ile Pro Gln Ser			

485	490	495	
Ser Lys Ser Gly Trp Ala Asn Pro Glu Arg Ala Val Arg Val Asn Ala			
500	505	510	
Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala Gly Leu Thr			
515	520	525	
Ile Thr Gly Glu Asp Ala Pro Asn Leu Lys Asn Ile Ala Phe His Glu			
530	535	540	
Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly Thr Asp Ala			
545	550	555	560
Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu Val			
565	570	575	
Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro Ser			
580	585	590	
Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu Ser			
595	600	605	
Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn Ala			
610	615	620	
Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp			
625	630	635	640
Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly			
645	650	655	
Glu Asn Asp Tyr Val Ala Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala			
660	665	670	
Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn			
675	680	685	
Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu			
690	695	700	

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Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys
705              710              715              720

Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg
              725              730              735

Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg
              740              745              750

Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro
              755              760              765

Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp
              770              775              780

Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys
785              790              795              800

Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala
              805              810              815

Val Lys Asn Glu Ala Lys Lys Lys
              820

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<213> Bacillus sp. KSM-S237

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<222> (1)..(2475)

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Met Met Leu Arg Lys Lys Thr Lys Gln Leu Ile Ser Ser Ile Leu Ile

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tta gtt tta ctt cta tct tta ttt ccg gca gct ctt gca gca gaa gga 96

Leu Val Leu Leu Leu Ser Leu Phe Pro Ala Ala Leu Ala Ala Glu Gly

20 25 30

aac act cgt gaa gac aat ttt aaa cat tta tta ggt aat gac aat gtt 144

Asn Thr Arg Glu Asp Asn Phe Lys His Leu Leu Gly Asn Asp Asn Val

35 40 45

aaa cgc cct tct gag gct ggc gca tta caa tta caa gaa gtc gat gga 192

Lys Arg Pro Ser Glu Ala Gly Ala Leu Gln Leu Gln Glu Val Asp Gly

50 55 60

caa atg aca tta gta gat caa cat gga gaa aaa att caa tta cgt gga 240

Gln Met Thr Leu Val Asp Gln His Gly Glu Lys Ile Gln Leu Arg Gly

65 70 75 80

atg agt aca cac gga tta cag tgg ttt cct gag atc ttg aat gat aac 288

Met Ser Thr His Gly Leu Gln Trp Phe Pro Glu Ile Leu Asn Asp Asn

85 90 95

gca tac aaa gct ctt tct aac gat tgg gat tcc aat atg att cgt ctt 336

Ala Tyr Lys Ala Leu Ser Asn Asp Trp Asp Ser Asn Met Ile Arg Leu

100	105	110	
gct atg tat gta ggt gaa aat ggg tac gct aca aac cct gag tta atc			384
Ala Met Tyr Val Gly Glu Asn Gly Tyr Ala Thr Asn Pro Glu Leu Ile			
115	120	125	
aaa caa aga gtg att gat gga att gag tta gcg att gaa aat gac atg			432
Lys Gln Arg Val Ile Asp Gly Ile Glu Leu Ala Ile Glu Asn Asp Met			
130	135	140	
tat gtt att gtt gac tgg cat gtt cat gcg cca ggt gat cct aga gat			480
Tyr Val Ile Val Asp Trp His Val His Ala Pro Gly Asp Pro Arg Asp			
145	150	155	160
cct gtt tat gca ggt gct aaa gat ttc ttt aga gaa att gca gct tta			528
Pro Val Tyr Ala Gly Ala Lys Asp Phe Phe Arg Glu Ile Ala Ala Leu			
165	170	175	
tac cct aat aat cca cac att att tat gag tta gcg aat gag ccg agt			576
Tyr Pro Asn Asn Pro His Ile Ile Tyr Glu Leu Ala Asn Glu Pro Ser			
180	185	190	
agt aat aat aat ggt gga gca ggg att ccg aat aac gaa gaa ggt tgg			624
Ser Asn Asn Asn Gly Gly Ala Gly Ile Pro Asn Asn Glu Glu Gly Trp			
195	200	205	
aaa gcg gta aaa gaa tat gct gat cca att gta gaa atg tta cgt aaa			672

Lys Ala Val Lys Glu Tyr Ala Asp Pro Ile Val Glu Met Leu Arg Lys

210

215

220

agc ggt aat gca gat gac aac att atc att gtt ggt agt cca aac tgg 720

Ser Gly Asn Ala Asp Asp Asn Ile Ile Ile Val Gly Ser Pro Asn Trp

225

230

235

240

agt cag cgt ccg gac tta gca gct gat aat cca att gat gat cac cat 768

Ser Gln Arg Pro Asp Leu Ala Ala Asp Asn Pro Ile Asp Asp His His

245

250

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aca atg tat act gtt cac ttc tac act ggt tca cat gct gct tca act 816

Thr Met Tyr Thr Val His Phe Tyr Thr Gly Ser His Ala Ala Ser Thr

260

265

270

gaa agc tat ccg tct gaa act cct aac tct gaa aga gga aac gta atg 864

Glu Ser Tyr Pro Ser Glu Thr Pro Asn Ser Glu Arg Gly Asn Val Met

275

280

285

agt aac act cgt tat gcg tta gaa aac gga gta gcg gta ttt gca aca 912

Ser Asn Thr Arg Tyr Ala Leu Glu Asn Gly Val Ala Val Phe Ala Thr

290

295

300

gag tgg gga acg agt caa gct agt gga gac ggt ggt cct tac ttt gat 960

Glu Trp Gly Thr Ser Gln Ala Ser Gly Asp Gly Gly Pro Tyr Phe Asp

305

310

315

320



gaa gca gat gta tgg att gaa ttt tta aat gaa aac aac att agc tgg 1008

Glu Ala Asp Val Trp Ile Glu Phe Leu Asn Glu Asn Asn Ile Ser Trp

325

330

335

gct aac tgg tct tta acg aat aaa aat gaa gta tct ggt gca ttt aca 1056

Ala Asn Trp Ser Leu Thr Asn Lys Asn Glu Val Ser Gly Ala Phe Thr

340

345

350

cca ttc gag tta ggt aag tct aac gca acc aat ctt gac cca ggt cca 1104

Pro Phe Glu Leu Gly Lys Ser Asn Ala Thr Asn Leu Asp Pro Gly Pro

355

360

365

gat cat gtg tgg gca cca gaa gaa tta agt ctt tct gga gaa tat gta 1152

Asp His Val Trp Ala Pro Glu Glu Leu Ser Leu Ser Gly Glu Tyr Val

370

375

380

cgt gct cgt att aaa ggt gtg aac tat gag cca atc gac cgt aca aaa 1200

Arg Ala Arg Ile Lys Gly Val Asn Tyr Glu Pro Ile Asp Arg Thr Lys

385

390

395

400

tac acg aaa gta ctt tgg gac ttt aat gat gga acg aag caa gga ttt 1248

Tyr Thr Lys Val Leu Trp Asp Phe Asn Asp Gly Thr Lys Gln Gly Phe

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410

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gga gtg aat tcg gat tct cca aat aaa gaa ctt att gca gtt gat aat 1296

Gly Val Asn Ser Asp Ser Pro Asn Lys Glu Leu Ile Ala Val Asp Asn

420

425

430

gaa aac aac act ttg aaa gtt tcg gga tta gat gta agt aac gat gtt 1344

Glu Asn Asn Thr Leu Lys Val Ser Gly Leu Asp Val Ser Asn Asp Val

435

440

445

tca gat ggc aac ttc tgg gct aat gct cgt ctt tct gcc aac ggt tgg 1392

Ser Asp Gly Asn Phe Trp Ala Asn Ala Arg Leu Ser Ala Asn Gly Trp

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455

460

gga aaa agt gtt gat att tta ggt gct gag aag ctt aca atg gat gtt 1440

Gly Lys Ser Val Asp Ile Leu Gly Ala Glu Lys Leu Thr Met Asp Val

465

470

475

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att gtt gat gaa cca acg acg gta gct att gcg gcg att cca caa agt 1488

Ile Val Asp Glu Pro Thr Thr Val Ala Ile Ala Ala Ile Pro Gln Ser

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495

agt aaa agt gga tgg gca aat cca gag cgt gct gtt cga gtg aac gcg 1536

Ser Lys Ser Gly Trp Ala Asn Pro Glu Arg Ala Val Arg Val Asn Ala

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510

gaa gat ttt gtc cag caa acg gac ggt aag tat aaa gct gga tta aca 1584

Glu Asp Phe Val Gln Gln Thr Asp Gly Lys Tyr Lys Ala Gly Leu Thr

515

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att aca gga gaa gat gct cct aac cta aaa aat atc gct ttt cat gaa 1632

Ile Thr Gly Glu Asp Ala Pro Asn Leu Lys Asn Ile Ala Phe His Glu

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gaa gat aac aat atg aac aac atc att ctg ttc gtg gga act gat gca			1680
Glu Asp Asn Asn Met Asn Asn Ile Ile Leu Phe Val Gly Thr Asp Ala			
545	550	555	560
gct gac gtt att tac tta gat aac att aaa gta att gga aca gaa gtt			1728
Ala Asp Val Ile Tyr Leu Asp Asn Ile Lys Val Ile Gly Thr Glu Val			
	565	570	575
gaa att cca gtt gtt cat gat cca aaa gga gaa gct gtt ctt cct tct			1776
Glu Ile Pro Val Val His Asp Pro Lys Gly Glu Ala Val Leu Pro Ser			
	580	585	590
gtt ttt gaa gac ggt aca cgt caa ggt tgg gac tgg gct gga gag tct			1824
Val Phe Glu Asp Gly Thr Arg Gln Gly Trp Asp Trp Ala Gly Glu Ser			
	595	600	605
ggt gtg aaa aca gct tta aca att gaa gaa gca aac ggt tct aac gcg			1872
Gly Val Lys Thr Ala Leu Thr Ile Glu Glu Ala Asn Gly Ser Asn Ala			
	610	615	620
tta tca tgg gaa ttt gga tat cca gaa gta aaa cct agt gat aac tgg			1920
Leu Ser Trp Glu Phe Gly Tyr Pro Glu Val Lys Pro Ser Asp Asn Trp			
625	630	635	640
gca aca gct cca cgt tta gat ttc tgg aaa tct gac ttg gtt cgc ggt			1968

Ala Thr Ala Pro Arg Leu Asp Phe Trp Lys Ser Asp Leu Val Arg Gly

645

650

655

gag aat gat tat gta gct ttt gat ttc tat cta gat cca gtt cgt gca 2016

Glu Asn Asp Tyr Val Ala Phe Asp Phe Tyr Leu Asp Pro Val Arg Ala

660

665

670

aca gaa ggc gca atg aat atc aat tta gta ttc cag cca cct act aac 2064

Thr Glu Gly Ala Met Asn Ile Asn Leu Val Phe Gln Pro Pro Thr Asn

675

680

685

ggg tat tgg gta caa gca cca aaa acg tat acg att aac ttt gat gaa 2112

Gly Tyr Trp Val Gln Ala Pro Lys Thr Tyr Thr Ile Asn Phe Asp Glu

690

695

700

tta gag gaa gcg aat caa gta aat ggt tta tat cac tat gaa gtg aaa 2160

Leu Glu Glu Ala Asn Gln Val Asn Gly Leu Tyr His Tyr Glu Val Lys

705

710

715

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att aac gta aga gat att aca aac att caa gat gac acg tta cta cgt 2208

Ile Asn Val Arg Asp Ile Thr Asn Ile Gln Asp Asp Thr Leu Leu Arg

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730

735

aac atg atg atc att ttt gca gat gta gaa agt gac ttt gca ggg aga 2256

Asn Met Met Ile Ile Phe Ala Asp Val Glu Ser Asp Phe Ala Gly Arg

740

745

750

gtc ttt gta gat aat gtt cgt ttt gag ggg gct gct act act gag ccg 2304

Val Phe Val Asp Asn Val Arg Phe Glu Gly Ala Ala Thr Thr Glu Pro

755

760

765

gtt gaa cca gag cca gtt gat cct ggc gaa gag acg cca cct gtc gat 2352

Val Glu Pro Glu Pro Val Asp Pro Gly Glu Glu Thr Pro Pro Val Asp

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775

780

gag aag gaa gcg aaa aaa gaa caa aaa gaa gca gag aaa gaa gag aaa 2400

Glu Lys Glu Ala Lys Lys Glu Gln Lys Glu Ala Glu Lys Glu Glu Lys

785

790

795

800

gaa gca gta aaa gaa gaa aag aaa gaa gct aaa gaa gaa aag aaa gca 2448

Glu Ala Val Lys Glu Glu Lys Lys Glu Ala Lys Glu Glu Lys Lys Ala

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810

815

gtc aaa aat gag gct aag aaa aaa taa

2475

Val Lys Asn Glu Ala Lys Lys Lys

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<210> 3

<211> 54

<212> DNA

<213> Artificial Sequence

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ccattcgagt tagctcacgc aaatcttgac ccag 34

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ccattcgagt tagctcgtgc aaatcttgac ccag 34

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<211> 31

<212> DNA

<213> Artificial Sequence

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